

1030301-0303030

ggc ctc cgg cac agc tac gac tgt ggg atc aag gga atg cag ctg ctg 144
Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu
35 40 45

gtg ttc ccc agg cca ggc cag act ctc cgc ttc aag gtg gtg gat gaa	192
Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu	
50 55 60	
ttt ggg aac cga ttt gat gtc aac aac tgc tcc atc tgc tac cac tgg	240
Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp	
65 70 75 80	
gtc acc tcc agg ccg cag gag cct gca gtc ttc tcg gcc gat tac aga	288
Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg	
85 90 95	
ggc tgc cac gtg ctg gag aag gat ggg cgt ttc cac ctg agg gtg ttc	336
Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe	
100 105 110	
atg gag gct gtg ctg ccc aat ggt cgt gtg gat gtg gca caa gac gct	384
Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala	
115 120 125	
act ctg atc tgt ccc aaa cct gac ccc tcc cgg act ctg gac tcc cag	432
Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln	
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ctg gca cca ccc gcc atg ttc tct gtc tca acc cca caa acc ctt tcc	480
Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln Thr Leu Ser	
145 150 155 160	
ttc ctc ccc acc tct ggc cat acc tcc caa ggc tct ggc cat gcc ttt	528
Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly His Ala Phe	
165 170 175	
ccc agc cca ctg gac cca ggg cac agc tct gtc cac cca acc cct gct	576
Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro Thr Pro Ala	
180 185 190	
tta cca tcc cct gga cct gga cct acc ctc gcc acc ctg gct caa ccc	624
Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu Ala Gln Pro	
195 200 205	
cac tgg ggc acc ttg gaa cac tgg gat gtg aac aaa cga gat tac ata	672
His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg Asp Tyr Ile	
210 215 220	

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Gly Thr His Leu Ser Gln Glu Gln Cys Gln Val Ala Ser Gly His Leu	
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ccc tgc atc gtg aga aga act tca aaa gaa gcc tgt cag cag gct ggc	768
Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln Gln Ala Gly	
245 250 255	
tgc tgc tat gac aac acc aga gag gtt ccc tgt tac tat ggc aac aca	816
Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr Gly Asn Thr	
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gct act gtc cag tgc ttc aga gat ggc tac ttc gtc ctc gta gtg tcc	864
Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu Val Val Ser	
275 280 285	
caa gaa atg gcc ttg aca cac agg atc aca ctg gcc aac atc cac ctg	912
Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn Ile His Leu	
290 295 300	
gcc tat gcc ccc acc agc tgc tcc cca aca cag cac acg gaa gct ttc	960
Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr Glu Ala Phe	
305 310 315 320	
gtg gtc ttc tac ttc cct ctc acc cac tgt gga acc aca atg cag gtg	1008
Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr Met Gln Val	
325 330 335	
gct ggc gac cag ctc atc tat gag aac tgg ctg gtg tct ggc atc cac	1056
Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser Gly Ile His	
340 345 350	
atc caa aag ggg cca cag ggt tcc atc acg cgg gac agc acc ttc cag	1104
Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser Thr Phe Gln	
355 360 365	
ctt cat gtg cgc tgt gtc ttc aac gcc agt gac ttc ctg ccc att cag	1152
Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu Pro Ile Gln	
370 375 380	

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Ala Ser Ile Phe Pro Pro Pro Ser Pro Ala Pro Met Thr Gln Pro Gly	
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Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr Cys Ser Ser	
405 410 415	
tac tat ggg gag gat gac tat ccc atc gtg agg ctg ctc cga gaa cca	1296
Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu Arg Glu Pro	
420 425 430	
gtc cat gtg gag gtc cgg ctt ctg cag agg aca gac ccc aac ctg gtc	1344
Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro Asn Leu Val	
435 440 445	
ctg ctg ctg cac cag tgc tgg ggc gct ccc agt gcc aac ccc ttc cag	1392
Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln	
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Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp	
465 470 475 480	
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Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln	
485 490 495	
tcg cac tac cag cga ttc act gtt gct acc ttc gcc ctc ctg gac tca	1536
Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser	
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Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr	
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tct gcc tgc cac acc tca ggg ctg gag act tgc tcc act gca tgt agc	1632
Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser	
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Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr	
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Gly	Leu	Arg	His	Ser	Tyr	Asp	Cys	Gly	Ile	Lys	Gly	Met	Gln	Leu	Leu
		35					40					45			
Val	Phe	Pro	Arg	Pro	Gly	Gln	Thr	Leu	Arg	Phe	Lys	Val	Val	Asp	Glu
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Phe	Gly	Asn	Arg	Phe	Asp	Val	Asn	Asn	Cys	Ser	Ile	Cys	Tyr	His	Trp
65					70					75					80
Val	Thr	Ser	Arg	Pro	Gln	Glu	Pro	Ala	Val	Phe	Ser	Ala	Asp	Tyr	Arg
				85					90					95	
Gly	Cys	His	Val	Leu	Glu	Lys	Asp	Gly	Arg	Phe	His	Leu	Arg	Val	Phe
			100					105					110		

Met	Glu	Ala	Val	Leu	Pro	Asn	Gly	Arg	Val	Asp	Val	Ala	Gln	Asp	Ala	115	120	125
Thr	Leu	Ile	Cys	Pro	Lys	Pro	Asp	Pro	Ser	Arg	Thr	Leu	Asp	Ser	Gln	130	135	140
Leu	Ala	Pro	Pro	Ala	Met	Phe	Ser	Val	Ser	Thr	Pro	Gln	Thr	Leu	Ser	145	150	155
Phe	Leu	Pro	Thr	Ser	Gly	His	Thr	Ser	Gln	Gly	Ser	Gly	His	Ala	Phe	165	170	175
Pro	Ser	Pro	Leu	Asp	Pro	Gly	His	Ser	Ser	Val	His	Pro	Thr	Pro	Ala	180	185	190
Leu	Pro	Ser	Pro	Gly	Pro	Gly	Pro	Thr	Leu	Ala	Thr	Leu	Ala	Gln	Pro	195	200	205
His	Trp	Gly	Thr	Leu	Glu	His	Trp	Asp	Val	Asn	Lys	Arg	Asp	Tyr	Ile	210	215	220
Gly	Thr	His	Leu	Ser	Gln	Glu	Gln	Cys	Gln	Val	Ala	Ser	Gly	His	Leu	225	230	235
Pro	Cys	Ile	Val	Arg	Arg	Thr	Ser	Lys	Glu	Ala	Cys	Gln	Gln	Ala	Gly	245	250	255
Cys	Cys	Tyr	Asp	Asn	Thr	Arg	Glu	Val	Pro	Cys	Tyr	Tyr	Gly	Asn	Thr	260	265	270
Ala	Thr	Val	Gln	Cys	Phe	Arg	Asp	Gly	Tyr	Phe	Val	Leu	Val	Val	Ser	275	280	285
Gln	Glu	Met	Ala	Leu	Thr	His	Arg	Ile	Thr	Leu	Ala	Asn	Ile	His	Leu	290	295	300
Ala	Tyr	Ala	Pro	Thr	Ser	Cys	Ser	Pro	Thr	Gln	His	Thr	Glu	Ala	Phe	305	310	315
Val	Val	Phe	Tyr	Phe	Pro	Leu	Thr	His	Cys	Gly	Thr	Thr	Met	Gln	Val	325	330	335
Ala	Gly	Asp	Gln	Leu	Ile	Tyr	Glu	Asn	Trp	Leu	Val	Ser	Gly	Ile	His	340	345	350
Ile	Gln	Lys	Gly	Pro	Gln	Gly	Ser	Ile	Thr	Arg	Asp	Ser	Thr	Phe	Gln	355	360	365
Leu	His	Val	Arg	Cys	Val	Phe	Asn	Ala	Ser	Asp	Phe	Leu	Pro	Ile	Gln	370	375	380
Ala	Ser	Ile	Phe	Pro	Pro	Pro	Ser	Pro	Ala	Pro	Met	Thr	Gln	Pro	Gly	385	390	395
Pro	Leu	Arg	Leu	Glu	Leu	Arg	Ile	Ala	Lys	Asp	Glu	Thr	Cys	Ser	Ser	405	410	415
Tyr	Tyr	Gly	Glu	Asp	Asp	Tyr	Pro	Ile	Val	Arg	Leu	Leu	Arg	Glu	Pro	420	425	430
Val	His	Val	Glu	Val	Arg	Leu	Leu	Gln	Arg	Thr	Asp	Pro	Asn	Leu	Val	435	440	445

09022480-080304

Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln
 450 455 460
 Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp
 465 470 475 480
 Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln
 485 490 495
 Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser
 500 505 510
 Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr
 515 520 525
 Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser
 530 535 540
 Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr
 545 550 555 560
 Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val Gly Phe Glu
 565 570 575
 Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp Ser Asn Gly
 580 585 590
 Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu Leu Pro Ala
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 Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu Ser Gln Thr
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<223> degenerate nucleotide sequence

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<223> n = A,T,C or G

<221> misc_feature

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<223> n = A,T,C or G

<221> misc_feature

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<223> n = A,T,C or G

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825, 837, 843, 852, 855, 858, 861, 864, 876, 879, 882, 888,
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<223> n = A,T,C or G

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<223> n = A,T,C or G

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<223> n = A,T,C or G

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1788, 1791, 1794, 1797, 1800, 1806, 1809, 1812, 1815, 1818,
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<223> n = A,T,C or G

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<222> 1851, 1857, 1860, 1863, 1866, 1872, 1878, 1887, 1896, 1902

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 <223> Oligonucleotide primer ZC29717

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